

O. Zaghmout

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/992,914A

DATE: 05/05/2000
TIME: 12:18:18

Input Set : A:\20-4348.txt
Output Set: N:\CRF3\05052000\H992914A.raw

3 <110> APPLICANT: WATANABE, Eihiro
4 OEDA, Kenji
6 <120> TITLE OF INVENTION: Raffinose Synthase Genes and Their Use
8 <130> FILE REFERENCE: 0020-4348P
10 <140> CURRENT APPLICATION NUMBER: 08/992,914A
11 <141> CURRENT FILING DATE: 1997-12-18
13 <150> PRIOR APPLICATION NUMBER: 8-338673/1996 JAPAN
14 <151> PRIOR FILING DATE: 1996-12-18
16 <160> NUMBER OF SEQ ID NOS: 87
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2746
22 <212> TYPE: DNA
23 <213> ORGANISM: Vicia faba
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (101)..(2497)
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32 gtcaataaagc tactaagcta ccagagtctc atcaatcacc atg gca cca cca agc 115
33 Met Ala Pro Pro Ser
34 1 5
36 ata acc aaa act gca acc ctc caa gac gta ata agc acc atc gat att 163
37 Ile Thr Lys Thr Ala Thr Leu Gln Asp Val Ile Ser Thr Ile Asp Ile
38 10 15 20
40 ggt aat ggt aac tca ccc tta ttc tcc ata acc tta gac caa tca cgt 211
41 Gly Asn Gly Asn Ser Pro Leu Phe Ser Ile Thr Leu Asp Gln Ser Arg
42 25 30 35
44 gac ttc ctt gca aat ggc cac cct ttc ctc acc caa gtc cca cct aac 259
45 Asp Phe Leu Ala Asn Gly His Pro Phe Leu Thr Gln Val Pro Pro Asn
46 40 45 50
48 ata aca aca aca aca acc act gct tcc tct ttt ctc aat ctc aaa 307
49 Ile Thr Thr Thr Thr Thr Thr Thr Ala Ser Ser Phe Leu Asn Leu Lys
50 55 60 65
52 tcc aac aaa gat acc att ccc aac aac aac acc atg ttg ttg caa 355
53 Ser Asn Lys Asp Thr Ile Pro Asn Asn Asn Asn Thr Met Leu Leu Gln
54 70 75 80 85
56 caa ggt tgt ttc gtt ggt ttc aac tcc acc gaa ccc aaa agc cac cac 403
57 Gln Gly Cys Phe Val Gly Phe Asn Ser Thr Glu Pro Lys Ser His His
58 90 95 100
60 gta gtt cca ctc ggc aaa cta aaa gga atc aaa ttc atg agc ata ttc 451
61 Val Val Pro Leu Gly Lys Leu Lys Gly Ile Lys Phe Met Ser Ile Phe
62 105 110 115
64 cgg ttc aaa gtt tgg tgg aca act cac tgg gtc gga aca aat gga cag 499
65 Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Thr Asn Gly Gln
66 120 125 130
68 gaa cta caa cac gaa aca caa atg tta atc ctg gac aaa aac gac tcc 547

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69 Glu Leu Gln His Glu Thr Gln Met Leu Ile Leu Asp Lys Asn Asp Ser
70      135      140      145
72 ctc gga cga ccc tat gtc tta ctc ctc cca atc cta gaa aac acc ttc 595
73 Leu Gly Arg Pro Tyr Val Leu Leu Leu Pro Ile Leu Glu Asn Thr Phe
74 150      155      160      165
76 cga acc tca ctc caa ccc ggt ctc aac gat cac ata ggc atg tcc gtc 643
77 Arg Thr Ser Leu Gln Pro Gly Leu Asn Asp His Ile Gly Met Ser Val
78      170      175      180
80 gaa agc ggt tca aca cat gtc acc ggg tca agc ttc aaa gca tgt ctt 691
81 Glu Ser Gly Ser Thr His Val Thr Gly Ser Ser Phe Lys Ala Cys Leu
82      185      190      195
84 tac atc cat ctc agt aac gac cca tac agt ata cta aaa gaa gca gtt 739
85 Tyr Ile His Leu Ser Asn Asp Pro Tyr Ser Ile Leu Lys Glu Ala Val
86      200      205      210
88 aaa gta atc caa act cag tta gga aca ttc aag act ctt gaa gaa aaa 787
89 Lys Val Ile Gln Thr Gln Leu Gly Thr Phe Lys Thr Leu Glu Glu Lys
90      215      220      225
92 aca gca cct agt att ata gac aaa ttc ggt tgg tgc acg tgg gat gct 835
93 Thr Ala Pro Ser Ile Ile Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala
94 230      235      240      245
96 ttt tac ttg aag gtt cat cca aaa ggt gta tgg gaa ggt gta aag tct 883
97 Phe Tyr Leu Lys Val His Pro Lys Gly Val Trp Glu Gly Val Lys Ser
98      250      255      260
100 ctc aca gat ggt ggt tgt cct ccc ggt ttc gtc ata atc gac gac ggt 931
101 Leu Thr Asp Gly Gly Cys Pro Pro Gly Phe Val Ile Ile Asp Asp Gly
102      265      270      275
104 tgg caa tcc att tgt cat gac gat gac gat gaa gat gat tca gga atg 979
105 Trp Gln Ser Ile Cys His Asp Asp Asp Asp Glu Asp Asp Ser Gly Met
106      280      285      290
108 aac cga acc tca gcc ggg gaa caa atg cca tgc aga ctt gta aaa tac 1027
109 Asn Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Val Lys Tyr
110      295      300      305
112 gaa gag aat tct aag ttt aga gaa tat gag aat cct gaa aat gga ggg 1075
113 Glu Glu Asn Ser Lys Phe Arg Glu Tyr Glu Asn Pro Glu Asn Gly Gly
114 310      315      320      325
116 aag aaa ggt ttg ggt ggt ttt gtg agg gat ttg aag gaa gag ttt ggg 1123
117 Lys Lys Gly Leu Gly Gly Phe Val Arg Asp Leu Lys Glu Glu Phe Gly
118      330      335      340
120 agt gtg gag agt gtt tat gtt tgg cat gcg ctt tgt ggg tat tgg ggc 1171
121 Ser Val Glu Ser Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly
122      345      350      355
124 ggg gtt agg cct gga gtg cat ggg atg ccg aaa gct agg gtt gtt gtt 1219
125 Gly Val Arg Pro Gly Val His Gly Met Pro Lys Ala Arg Val Val Val
126      360      365      370
128 ccg aag gtg tct cag ggg ttg aag atg acg atg gag gat ttg gcg gtg 1267
129 Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met Glu Asp Leu Ala Val
130      375      380      385
132 gat aag att gtt gag aac ggt gtg ggg cta gtg ccg cca gat ttt gca 1315
133 Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val Pro Pro Asp Phe Ala

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134	390		395		400		405		
136	cat	gag	atg	ttt	gat	ggg	ctt	cac	tct
137	His	Glu	Met	Phe	Asp	Gly	Leu	His	Ser
138					410				415
140	gac	ggt	gtt	aaa	ggt	gat	gtt	atc	cat
141	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His
142					425				430
144	gaa	tat	ggt	gga	cga	gtt	gag	cta	aga
145	Glu	Tyr	Gly	Gly	Arg	Val	Glu	Leu	Ala
146					440				445
148	acc	tca	tca	gtg	aag	aaa	cat	ttc	aaa
149	Thr	Ser	Ser	Val	Lys	Lys	His	Phe	Lys
150					455				460
152	atg	gag	cat	tgc	aac	gac	ttc	ctc	ctc
153	Met	Glu	His	Cys	Asn	Asp	Phe	Phe	Leu
154	470				475				480
156	ctc	ggc	cgc	gtc	gga	gat	gat	ttt	tgg
157	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp
158					490				495
160	cca	aat	ggt	aca	tat	tgg	ctc	caa	ggt
161	Pro	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly
162					505				510
164	tac	aac	agt	tta	tgg	atg	gga	aat	ttc
165	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe
166					520				525
168	ttt	cag	tcc	act	cat	cct	tgt	gct	gaa
169	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu
170					535				540
172	ata	tcc	ggc	gga	cca	att	tat	gtt	agt
173	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser
174	550				555				560
176	ttc	aag	ttg	ctc	aaa	tct	ctt	gtt	ttg
177	Phe	Lys	Leu	Leu	Lys	Ser	Leu	Val	Leu
178					570				575
180	tgt	caa	cat	tac	gca	ctc	cct	aca	aga
181	Cys	Gln	His	Tyr	Ala	Leu	Pro	Thr	Arg
182					585				590
184	ttg	cat	aat	ggc	aaa	aca	atg	ctg	aaa
185	Leu	His	Asn	Gly	Lys	Thr	Met	Leu	Lys
186					600				605
188	aca	ggt	gtt	ttg	ggt	ctt	ttc	aac	tgc
189	Thr	Gly	Val	Leu	Gly	Leu	Phe	Asn	Cys
190					615				620
192	gag	gca	cgg	cga	aac	aag	agt	gta	tct
193	Glu	Ala	Arg	Arg	Asn	Lys	Ser	Val	Ser
194	630				635				640
196	tgt	tat	gca	agt	ccc	gaa	gac	att	gaa
197	Cys	Tyr	Ala	Ser	Pro	Glu	Asp	Ile	Glu
198					650				655

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200 atg agc acc aaa ggt gtg gat ttt ttt gct gtg tat ttt ttc aag gag 2131
201 Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val Tyr Phe Phe Lys Glu
202 665 670 675
204 aag aaa ttg agg ctc atg aag tgt tct gat aga ttg aaa gtt tcg ctt 2179
205 Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg Leu Lys Val Ser Leu
206 680 685 690
208 gag cca ttt agt ttt gag cta atg aca gtg tct cca gtg aaa gtg ttt 2227
209 Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser Pro Val Lys Val Phe
210 695 700 705
212 tcg aaa agg ttt ata cag ttt gca ccg att ggg tta gtg aac atg ctg 2275
213 Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu
214 710 715 720 725
216 aac tct ggt ggt gcg att cag tct ctg gag ttt gat gat aat gca agt 2323
217 Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe Asp Asp Asn Ala Ser
218 730 735 740
220 ttg gtc aag att ggg gtg aga ggt tgc ggg gag atg agc gtg ttt gcg 2371
221 Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Ser Val Phe Ala
222 745 750 755
224 tct gag aaa ccg gtt tgc tgc aaa att gat ggg gtt aag gtg aaa ttt 2419
225 Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly Val Lys Val Lys Phe
226 760 765 770
228 ctt tat gag gac aaa atg gca aga gtt caa att ctg tgg cct agt tct 2467
229 Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile Leu Trp Pro Ser Ser
230 775 780 785
232 tca aca ttg tct ttg gtc cag ttt tta ttt tgatccctag gaatcctatg 2517
233 Ser Thr Leu Ser Leu Val Gln Phe Leu Phe
234 790 795
236 cacgtgtctc tgttacaag tactttatat aagtataata tgtatctatt tccattttta 2577
238 actgtcttta tgcaattagg tggtaatta gttatttgtt tgtgaagtaa ctaacttgc 2637
240 tgtgttgtaa gcttataata tatggtaag ttctcactt gtatatacct gttgtatgta 2697
242 taaattttac tatatatgac taacatcatt atcttgtgag caaaaaaaaa 2746
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247 <212> TYPE: PRT
248 <213> ORGANISM: Vicia faba
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252 1 5 10 15
254 Ser Thr Ile Asp Ile Gly Asn Gly Asn Ser Pro Leu Phe Ser Ile Thr
255 20 25 30
257 Leu Asp Gln Ser Arg Asp Phe Leu Ala Asn Gly His Pro Phe Leu Thr
258 35 40 45
260 Gln Val Pro Pro Asn Ile Thr Thr Thr Thr Thr Thr Thr Ala Ser Ser
261 50 55 60
263 Phe Leu Asn Leu Lys Ser Asn Lys Asp Thr Ile Pro Asn Asn Asn Asn
264 65 70 75 80
266 Thr Met Leu Leu Gln Gln Gly Cys Phe Val Gly Phe Asn Ser Thr Glu
267 85 90 95
269 Pro Lys Ser His His Val Val Pro Leu Gly Lys Leu Lys Gly Ile Lys

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270          100          105          110
272 Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val
273          115          120          125
275 Gly Thr Asn Gly Gln Glu Leu Gln His Glu Thr Gln Met Leu Ile Leu
276          130          135          140
278 Asp Lys Asn Asp Ser Leu Gly Arg Pro Tyr Val Leu Leu Leu Pro Ile
279 145          150          155          160
281 Leu Glu Asn Thr Phe Arg Thr Ser Leu Gln Pro Gly Leu Asn Asp His
282          165          170          175
284 Ile Gly Met Ser Val Glu Ser Gly Ser Thr His Val Thr Gly Ser Ser
285          180          185          190
287 Phe Lys Ala Cys Leu Tyr Ile His Leu Ser Asn Asp Pro Tyr Ser Ile
288          195          200          205
290 Leu Lys Glu Ala Val Lys Val Ile Gln Thr Gln Leu Gly Thr Phe Lys
291          210          215          220
293 Thr Leu Glu Glu Lys Thr Ala Pro Ser Ile Ile Asp Lys Phe Gly Trp
294 225          230          235          240
296 Cys Thr Trp Asp Ala Phe Tyr Leu Lys Val His Pro Lys Gly Val Trp
297          245          250          255
299 Glu Gly Val Lys Ser Leu Thr Asp Gly Gly Cys Pro Pro Gly Phe Val
300          260          265          270
302 Ile Ile Asp Asp Gly Trp Gln Ser Ile Cys His Asp Asp Asp Glu
303          275          280          285
305 Asp Asp Ser Gly Met Asn Arg Thr Ser Ala Gly Glu Gln Met Pro Cys
306          290          295          300
308 Arg Leu Val Lys Tyr Glu Glu Asn Ser Lys Phe Arg Glu Tyr Glu Asn
309 305          310          315          320
311 Pro Glu Asn Gly Gly Lys Lys Gly Leu Gly Gly Phe Val Arg Asp Leu
312          325          330          335
314 Lys Glu Glu Phe Gly Ser Val Glu Ser Val Tyr Val Trp His Ala Leu
315          340          345          350
317 Cys Gly Tyr Trp Gly Gly Val Arg Pro Gly Val His Gly Met Pro Lys
318          355          360          365
320 Ala Arg Val Val Val Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met
321          370          375          380
323 Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val
324 385          390          395          400
326 Pro Pro Asp Phe Ala His Glu Met Phe Asp Gly Leu His Ser His Leu
327          405          410          415
329 Glu Ser Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu
330          420          425          430
332 Glu Leu Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Arg Ala
333          435          440          445
335 Tyr Tyr Lys Ala Leu Thr Ser Ser Val Lys Lys His Phe Lys Gly Asn
336          450          455          460
338 Gly Val Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly
339 465          470          475          480
341 Thr Glu Ala Ile Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser
342          485          490          495

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/05/2000

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Input Set : A:\20-4348.txt

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L:542 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:542 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:1563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1738 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:1738 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:1738 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:48
L:1751 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49
L:1751 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:1751 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:49
L:1764 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:1764 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:1764 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:50
L:1777 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:1777 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:1777 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:51
L:1790 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:1790 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:1790 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
L:1917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:2085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:2103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76